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Volume III

THE TEXTS, POLITICAL HISTORY AND
ADMINISTRATION

Till c. 200 BC

Editors

Dilip K. Chakrabarti and Makkhan Lal



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I.3. Genetics and the Aryan Issue

Editorial Note

[There cannot be anything more unpleasant in the study of human affairs than the concept of race and the enormous literature built around it. The modern DNA studies have cast doubt on the validity of many of the earlier assumptions, and in this paper Danino demonstrates how the notion of the Aryans has not been supported by these studies in any way. This paper by Danino also provides an excellent introduction to the relevant DNA literature, including the opinions of M. Bamshad, P. Majumdar and others who seem to be keen on justifying the nineteenth century assumptions of race and language through something as sophisticated as molecular biology. He, however, makes it abundantly clear through his literature review that such attempts are thoroughly belied by the researches of scholars like Oppenheim, Kivisild, Sahoo, Sengupta, Raychaudhuri and many others.]

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BACKGROUND

Until the mid-twentieth century, anthropology was rooted in the concept of race. It took World War II and the horrors perpetrated in the name of an Aryan *Herrenfolk* for racial—and, generally, racist—theories to collapse. Rather late in the day, anthropologists realized that race cannot be scientifically defined, setting at naught over a century of scholarly divagations on “superior” and “inferior” races. Following in the footsteps of pioneers like Franz Boas (1912), scientists such as Ashley Montagu (1942) now strongly criticized the “fallacy of race”.

Despite notable exceptions (e.g., Datta 1935), Indian anthropologists, building on nineteenth-century work (especially that of H.H.

Risley, see Trautmann 1997; Chakrabarti 1997), went on listing imaginary Indian races—including the fabled Aryan and Dravidian races—for a few more decades, and indeed some of them occasionally linger on in today's history textbooks. Until the 1960s, for example, skeletal studies from Mohenjodaro and Harappa found it natural to stick colourful labels on the different "races" supposedly going into the composition of the Harappan population: Caucasoid, Mediterranean, Caspian, Proto-Australoid, Mongoloid, etc. (Sewell & Guha 1931; Bose et al. 1962) Such a method, or lack of it, left unanswered the big question at the heart of the Aryan debate in India: Could the hypothesis of the entry into the subcontinent of a new people (since we will henceforth shun the word "race") in the 2nd millennium BC be proved or disproved on biological grounds?

Only from about the 1970s did non-racial anthropological work begin to provide reliable leads on India's protohistory. Revisiting the skeletal data, Pratap C. Dutta (of the Anthropological Survey of India) found that however great the Harappans' internal diversity may have been, there was "a genetic continuum between the Harappans and the present-day people of the region." (Dutta 1984: 73) While Dutta refrained from drawing further conclusions, S.R. Walimbe was more forthcoming:

Reassessment of the [Harappan] skeletal record strongly indicates that the hypothesis of identification of "foreign" phenotypic element or unceremonious slaughter of native Harappans is not supplemented by bone evidence. (Walimbe 1993: 113)

Walimbe's conclusion was partly based on the work of Kenneth Kennedy (1982, 1984) who had refuted, on the ground of a careful skeletal

study, Mortimer Wheeler's claim that skeletons found in the streets of Mohenjodaro were evidence of a massacre by invading Aryans. In further research, Kennedy questioned the whole Aryan construct from an anthropological standpoint, calling the said Aryans "illusory" (Kennedy 1999: 182) and asking, "How could one recognize an Aryan, living or dead, when the biological criteria for Aryanness are non-existent?" (Kennedy 1995: 61) His conclusion was emphatic:

Biological anthropologists remain unable to lend support to any of the theories concerning an Aryan biological or demographic entity.... What the biological data demonstrate is that no exotic races are apparent from laboratory studies of human remains excavated from any archaeological sites.... All prehistoric human remains recovered thus far from the Indian subcontinent are phenotypically identifiable as ancient South Asians.... In short, there is no evidence of demographic disruptions in the north-western sector of the subcontinent during and immediately after the decline of the Harappan culture. (Kennedy 1995: 60, 54)

The last statement rules out the arrival of a new people in the 2nd millennium BC as envisaged by the Aryan scenario. It was endorsed by other experts, such as Brian Hemphill and John Lukacs (Hemphill et al. 1991, 1997), who found only two pre-and protohistoric discontinuities in the populations of the Indus Valley, especially its western and northern fringes: "The first occurs between 6000 and 4500 BC... [with] another discontinuity at some point after 800 BC but before 200 BC." (Hemphill et al. 1991: 174) If, then, the biological continuity extends from 4500 to 800 BC, it again leaves no room for any mass immigration around 1500 BC.

Such conclusions are implicitly endorsed in a 2007 study led by Jay T. Stock, which observes

a general level of homogeneity among the South Asian samples.... An analysis of South Asian cranial morphology in the context of the global pattern of human variation suggests that populations of the Indian subcontinent have a relatively unique and homogenous pattern of cranial morphology.... [This] suggests that, independent of whether or not there was an important demographic event in the mid-Holocene [i.e., c. 4000 BC], there was relatively little gene flow from outside of south Asia afterwards. (Stock et al. 2007: 257, 262)

The study also finds that “the tribal/nontribal boundary has been genetically more fluid than generally thought” (Stock et al. 2007: 262), an important observation which, as we will see, will be amply confirmed by genetics studies.

In 2007, too, Walimbe showed the pitfalls of interpreting changes in cranial shapes in terms of foreign gene flow, and concluded:

Cranial and dental morphological data clearly indicate genetic continuity from the Mesolithic era. The hypotheses regarding massive population movements during the protohistoric period cannot be supported on available skeletal data. (Walimbe 2007: 315)

Turning to archaeology, it is now well accepted that there is no sign in the Northwest of an intrusive material culture in the 2nd millennium BC (Bryant 2001; Chakrabarti 2008; Danino 2006b; Danino 2010; Gupta 1996; Jarrige 1995; Kenoyer 1998; Lal 1998; Lal 2002; Shaffer 1984). This double invisibility—archaeological and biological—has compelled die-hard proponents of the invasion / migration scenario to downscale it to a “trickle-in” infiltration (Witzel 2001), limited enough to have left no physical traces. But they are at pains to explain how such a “trickle” could have radically altered India’s linguistic and cultural landscape, when far more

sizeable invasions of the historical period failed to do so. More logically, other scholars still insist that “the Indo-Aryan immigrants seem to have been numerous and strong enough to continue and disseminate much of their culture” (Sharma 2001: 52), but they now find themselves on the wrong side of archaeological and biological evidence.

A POWERFUL NEW TOOL

The last two decades have seen the entry of genetics into the arena. While it may be argued that bioanthropologists could have missed a few tell-tale skulls, Indian populations still carry genetic markers which, one day, will enable us to reconstitute the history of their settling in India in fairly complete detail. In the meantime, important results have come to light.

In trying to reconstruct ancestry, biologists use two types of DNA, the complex molecule that carries genetic information. The first, Y-DNA, is contained in the Y-chromosome, one of the two sex chromosomes; it is found in the cell’s nucleus and is transmitted from father to son. The second, mtDNA or mitochondrial DNA, is found in mitochondria, kinds of power generators found in the cell, but outside its nucleus; this mtDNA is independent of the Y-DNA, simpler in structure, and transmitted by the mother alone (to her male or female child). For various reasons, all this genetic material undergoes slight alterations or “mutations” in the course of time; those mutations then become characteristic of the line of descendants and are called “genetic markers”. If, for instance, the mtDNAs of two humans, however distant geographically, exhibit the same mutation, they necessarily share a common ancestor in the maternal line.

Much of the difficulty lies in grouping genetic markers that share the same sets of

mutations into “haplotypes” (from a Greek word meaning “single”), genetic fingerprints of sorts that have found a wide array of applications, from therapeutics to crime detection to genealogy. Similar haplotypes are then brought together into “haplogroups”—not to be confused with the old notion of “race”. Such genetic markers can then be used to establish a “genetic distance” between two individuals or two populations.

Identifying and making sense of the right genetic markers is not the only difficulty; dating their mutations remains a major challenge: a marker of Y-DNA may undergo one mutation every 250 to 500 generations, which is not too precise. Genetics, therefore, needs inputs from palaeontology and archaeology, among other disciplines, to verify its historical conclusions. With their help, it becomes tempting to turn human genetic variation into actual history. Several ambitious attempts at a comprehensive story of human prehistoric migrations have come out in recent years, including “classics” such as L.L. Cavalli-Sforza’s *Genes, Peoples, and Languages* (2000), Stephen Oppenheimer’s *The Real Eve: Modern Man’s Journey Out of Africa* (2004) or Spencer Wells’s *The Journey of Man: A Genetic Odyssey* (2004).

INDIA’S CASE

Since the 1990s, there have been numerous genetic studies of Indian populations, often reaching apparently divergent conclusions. There are at least three reasons for this: (1) the Indian region happens to be the most genetically diverse in the world after Africa, which makes the interpretation of the data a complex and delicate exercise; (2) early studies relied on small samples, while thousands are required for statistical reliability; (3) some of the studies fall into the trap of trying to equate linguistic groups

with distinct ethnic entities—a relic of the nineteenth-century erroneous identification between language and race; as a result, a genetic connection between north Indians and Central Asians has automatically been taken to confirm an Aryan immigration in the 2nd millennium BC, disregarding a number of alternative explanations. We will return to these pitfalls.

More recent studies, using larger samples and more refined methods of analysis, both at the conceptual level and in the laboratory, have often reached very different conclusions. One of the first such studies, in 1999, was conducted by a team directed by the Estonian biologist Toomas Kivisild (who will be associated as author or co-author with many of the studies cited below); it relied on 550 samples of mtDNA and identified a haplogroup “U” as indicating a deep connection between Indian and West-Eurasian populations. However, the authors opted for a very remote separation of the two branches rather than a recent population movement towards India; in fact, “the subcontinent served as a pathway for eastward migration of modern humans” from Africa some 40,000 years ago:

We found an extensive deep late Pleistocene genetic link between contemporary Europeans and Indians, provided by the mtDNA haplogroup U, which encompasses roughly a fifth of mtDNA lineages of both populations. Our estimate for this split [between Europeans and Indians] is close to the suggested time for the peopling of Asia and the first expansion of anatomically modern humans in Eurasia and likely pre-dates their spread to Europe. (Kivisild et al. 1999: 1331)

In other words, the genetic affinity between the Indian subcontinent and Europe “should not be interpreted in terms of a recent admixture of western Caucasoids with Indians caused by a

putative Indo-Aryan invasion 3,000–4,000 years BP [before present].” (Kivisild et al. 1999: 1333) This was probably the first major challenge to the invasionist model arising out of genetics.

The second was published just a month later. Authored by the U.S. biological anthropologist Todd R. Disotell, the study dealt with the first migration of modern man from Africa towards Asia, and found that migrations into India “did occur, but rarely from western Eurasian populations.” Disotell made observations very similar to those of the preceding paper:

The supposed Aryan invasion of India 3,000–4,000 years before present therefore did not make a major splash in the Indian gene pool. This is especially counter-indicated by the presence of equal, though very low, frequencies of the western Eurasian mtDNA types in both southern and northern India. Thus, the “caucasoid” features of south Asians may best be considered “pre-caucasoid” — that is, part of a diverse north or north-east African gene pool that yielded separate origins for western Eurasian and southern Asian populations over 50,000 years ago. (Disotell 1999: R926)

Here again, the Eurasian connection is traced to the original migration out of Africa, so that “the supposed Aryan invasion of India 3000–4000 years ago was much less significant than is generally believed.” (Disotell 1999: R925)

GENES, RELIGION, CASTE AND LANGUAGE

A year later, thirteen Indian scientists led by Susanta Roychoudhury studied 644 samples of mtDNA from some ten Indian ethnic groups, especially from the East and South. They found “a fundamental unity of mtDNA lineages in India, in spite of the extensive cultural and linguistic diversity”, pointing to “a relatively small founding group of females in India.”

(Roychoudhury et al. 2000: 1190) Significantly, most of the mtDNA diversity observed in Indian populations is between individuals within populations; there is no significant structuring of haplotype diversity by socio-religious affiliation, geographical location of habitat or linguistic affiliation. (Roychoudhury et al. 2000: 1187).

That is a crucial observation, which later studies will endorse: on the maternal side at least, and in the regions studied, there is no such thing as a “Hindu” or “Muslim” genetic identity, nor also a high- or low-caste one—hence the paper’s title: “Fundamental genomic unity of ethnic India is revealed by analysis of mitochondrial DNA.” The authors also noted that haplogroup “U”, already noted by Kivisild et al. (1999) as being common to north Indian and “Caucasoid” populations, was found in tribes of eastern India such as the Lodhas and Santals. This would not be the case if it had been introduced through Indo-Aryans. Such is also the case of the haplogroup “M”, another marker frequently mentioned in the early literature as evidence of the invasion: in reality, “We have now shown that indeed haplogroup *M* occurs with a high frequency, averaging about 60%, across most Indian population groups, irrespective of geographical location of habitat. We have also shown that the tribal populations have higher frequencies of haplogroup *M* than caste populations.” (Roychoudhury et al. 2000: 1189)

Also in 2000, twenty authors headed by Kivisild contributed a chapter to a book on Europe’s archaeogenetics. They first stressed the importance of the mtDNA haplogroup “M” common to India (with a frequency of 60%), central and eastern Asia (40% on average), and even to American Indians; however, this frequency drops to 0.6% in Europe, which is

“inconsistent with the ‘general Caucasoidness’ of Indians.” This shows, once again, that “the Indian maternal gene pool has come largely through an autochthonous history since the Late Pleistocene” (Kivisild et al. 2000: 271), in other words, before some 15,000 years ago. Looking at mtDNA as a whole, the paper stated, “Even the high castes share more than 80 per cent of their maternal lineages with the lower castes and tribals” (Kivisild et al. 2000: 271), which also runs counter to the invasionist thesis. Taking all aspects into consideration, the authors’ conclusion was:

We believe that there are now enough reasons not only to question a “recent Indo–Aryan invasion” into India some 4000 BP, but alternatively to consider India as a part of the common gene pool ancestral to the diversity of human maternal lineages in Europe. (Kivisild et al. 2000: 267)

In 2003, Kivisild published two more studies. The first dealt with the origin of languages and agriculture in India and stressed India’s genetic complexity and antiquity, since “present-day Indians [possess] at least 90 per cent of what we think of as autochthonous Upper Palaeolithic maternal lineages.” (Kivisild et al. 2003a: 221) The authors noted:

The Indian mtDNA tree in general [is] not subdivided according to linguistic (Indo-European, Dravidian) or caste affiliations, although there may occur (sometimes drastic) population-wise differences in frequencies of particular sub-clusters. (Kivisild et al. 2003a: 216)

This again highlights the old error of conflating language and race or ethnic group: there is no “Hindi-speaker gene” or “Tamil-speaker gene”, and again no “upper-caste gene” or “low-caste gene”, despite entrenched misconceptions still prevalent in this regard.

The second study, a particularly detailed one dealing with the genetic heritage of India’s earliest settlers, relied on nearly a thousand samples from the subcontinent, including two Dravidian-speaking tribes from Andhra Pradesh. Among other findings, it stressed that the Y-DNA haplogroup M17, regarded till recently as a genetic marker for an Indo-Aryan migration, and indeed frequent in Central Asia, is equally found in the two tribes under consideration, which is inconsistent with the invasionist framework. Moreover, one of the two tribes, the Chenchus, is genetically close to several castes, so that there is a “lack of clear distinction between Indian castes and tribes” (Kivisild et al. 2003b: 329)—fact that can hardly be overemphasized.

This also emerges from a study of genetic distances between eight Indian and seven Eurasian populations. These distances, calculated on the basis of 16 Y-DNA haplogroups (Fig. 1), challenge many common assumptions: not only are the Chenchus close to five castes, as just mentioned, but we find another tribe, the Lambadis (probably of Rajasthani origin), stuck between western Europe and the Middle East, Bengalis of various castes close to Mumbai Brahmins, and Goan Brahmins and Punjabis (both of whom one would have expected to be closest to Central Asia (assuming an Aryan immigration) as far away as possible from it. It becomes clear that no simple framework can account for such complexity.

The next year, a study directed by Mait Metspalu analyzed 796 Indian (including tribal and caste populations from different parts of India) and 436 Iranian mtDNAs. Of relevance to our purpose is the following observation:

Language families present today in India, such as Indo-European, Dravidic and Austro-Asiatic, are all

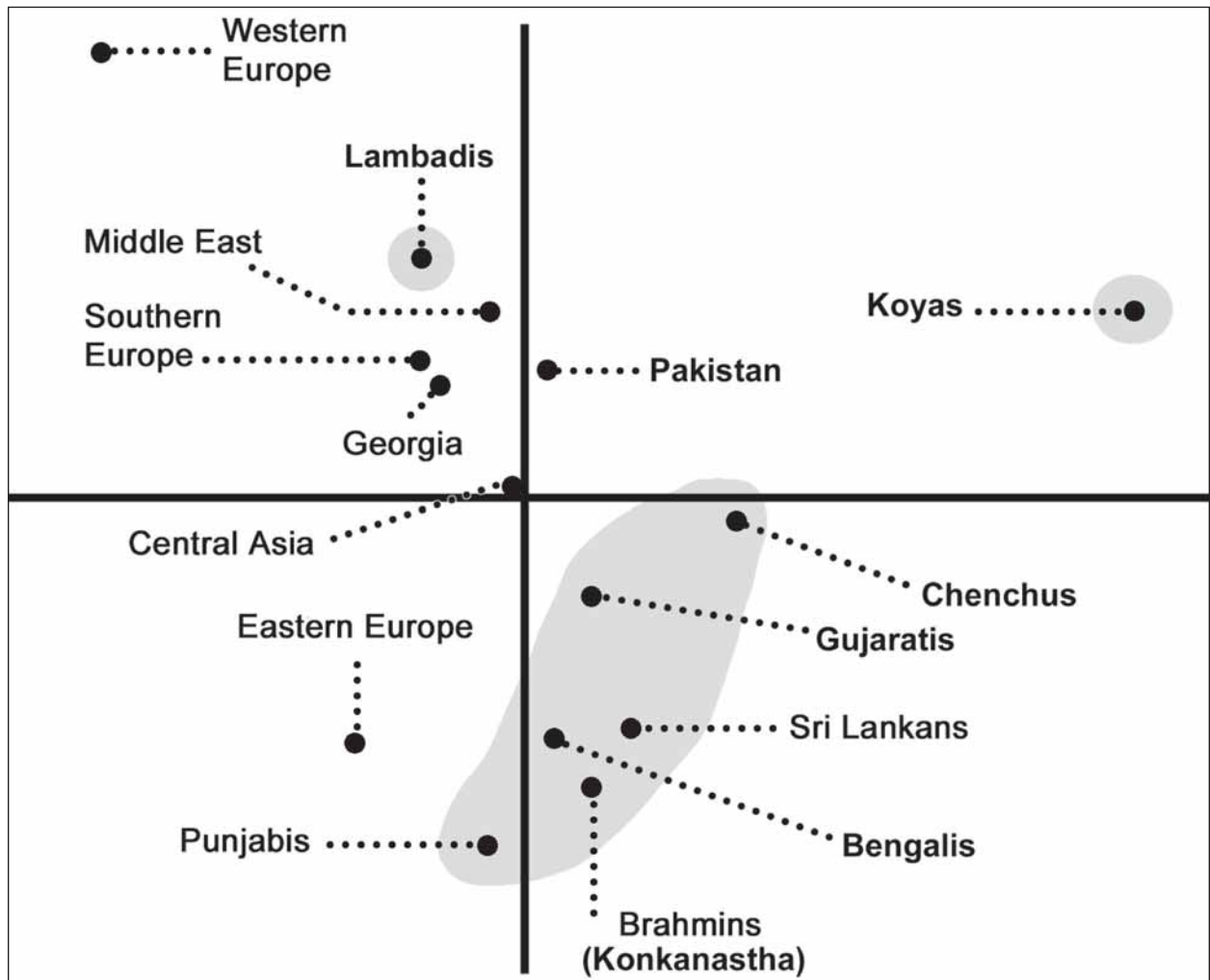


Fig. 1. Genetic distances between eight Indian and seven western Eurasian populations, calculated for 16 Y-DNA haplogroups (adapted from Kivisild et al. 2003b: 325).

much younger than the majority of indigenous mtDNA lineages found among their present-day speakers at high frequencies. It would make it highly speculative to infer, from the extant mtDNA pools of their speakers, whether one of the listed above linguistically defined group in India should be considered more “autochthonous” than any other in respect of its presence in the subcontinent. (Metspalu et al. 2004)

Thus, Indian populations probably spoke now extinct languages when they settled in India; the current language families—Indo-

European, Dravidian, Austro-Asiatic and Tibeto-Burmese being the main ones—took shape later, without requiring massive population displacements. The authors do find traces of an “Eurasian contribution” to the Indian maternal gene pool, but they attribute it partly to a “large-scale” immigration some 40,000 years ago, and partly to “relatively low-intensity long-lasting admixture at the border regions as well as a consequence of numerous but probably limited migrations during the last 10,000 ybp [years

before present].” (Metspalu et al. 2004) In conclusion, the authors see:

a genetic continuum that spans from the Near East into India extending north into Central Asia. The coalescence times of these haplogroups suggest that this continuum took shape somewhere between 30,000 to 50,000 ybp, thus falling within the climatically favorable interglacial period. We notice that the extant U7 and W frequencies along the proposed continuum are not uniform. U7 is more predominant in Iran, Pakistan, northwestern India and the Arabian peninsula, while W is more frequent in the western Near-East, Anatolia and the Caucasus. The coalescence ages of the Indian- and Iranian-specific U7 clades suggest that the time-window of this continuum was closed by ca. 20,000 ybp. (Metspalu et al. 2004)

If so, the main genetic connection between northwest India and Iran, would date to before 20,000 years ago, and would not be attributable to a recent split between Indo-Aryans and Irano-Aryans.

CENTRAL ASIA; DRAVIDIAN SPEAKERS; CASTE-TRIBE CONTINUUM

Three studies relevant to our investigation appeared in 2006. The first was headed by the Indian biologist Sanghamitra Sengupta. Based on 728 samples covering 36 Indian populations, it announced in its very title how its findings revealed a “Minor Genetic Influence of Central Asian Pastoralists”, i.e. of supposed Indo-Aryans, and stated its general agreement with the previous study. For instance, the authors rejected the identification of some Y-DNA genetic markers with an “Indo-European expansion”, an identification they called “convenient but incorrect... overly simplistic.” (Sengupta et al. 2006: 217-18) To them, the subcontinent’s genetic landscape was formed much earlier than the dates proposed for an

Indo-Aryan immigration: “The influence of Central Asia on the pre-existing gene pool was minor. ... There is no evidence whatsoever to conclude that Central Asia has been necessarily the recent donor and not the receptor of the R1a lineages.” (Sengupta et al. 2006: 218; the R1a lineages being a different way to denote the haplogroup M17).

Finally, and significantly, this study indirectly rejected a “Dravidian” authorship of the Indus-Sarasvati Civilization, since it noted, “Our data are also more consistent with a peninsular origin of Dravidian speakers than a source with proximity to the Indus....” (Sengupta et al. 2006: 202) They found, in conclusion, “overwhelming support for an Indian origin of Dravidian speakers.” (Sengupta et al. 2006: 219) This runs counter to a popular but merely speculative thesis that the Harappans were basically “Dravidians”, a thesis which archaeology also fails to support (Danino 2009).

Another Indian biologist, Sanghamitra Sahoo, headed a study of the Y-DNA of 936 samples covering 77 Indian populations, 32 of them tribes. Their work confirmed earlier findings: “The sharing of some Y-chromosomal haplogroups between Indian and Central Asian populations is most parsimoniously explained by a deep, common ancestry between the two regions, with diffusion of some Indian-specific lineages northward.” (Sahoo et al. 2006: 843) So the southward gene flow that had been imprinted on our minds for two centuries may turn out to be wrong: it appears that early population flow was out of, not into, India. The authors continue:

The Y-chromosomal data consistently suggest a largely South Asian origin for Indian caste communities and therefore argue against any major influx, from regions north and west

	North castes	South castes	Reduced tribes	Northeast- east tribes	Turkey	Central Asia	Mongols/ Buryats	Southeast Asia	Iran	Iraq	East Europe	Russia	West Europe	Ethiopia
North castes	0.00													
South castes	0.07	0.00												
Reduced tribes	0.06	0.05	0.00											
Northeast-east tribes	0.21	0.20	0.19	0.00										
Turkey	0.11	0.14	0.13	0.21	0.00									
Central Asia	0.07	0.12	0.10	0.19	0.05	0.00								
Mongols/Buryats	0.26	0.27	0.26	0.32	0.21	0.12	0.00							
Southeast Asia	0.26	0.27	0.26	0.21	0.22	0.19	0.30	0.00						
Iran	0.09	0.12	0.11	0.22	0.01	0.06	0.24	0.24	0.00					
Iraq	0.16	0.19	0.17	0.26	0.04	0.10	0.27	0.27	0.02	0.00				
East Europe	0.08	0.23	0.19	0.33	0.16	0.11	0.34	0.34	0.18	0.23	0.00			
Russia	0.08	0.20	0.16	0.29	0.11	0.06	0.28	0.30	0.13	0.18	0.03	0.00		
West Europe	0.26	0.29	0.25	0.35	0.14	0.17	0.36	0.36	0.22	0.23	0.28	0.19	0.00	
Ethiopia	0.31	0.33	0.32	0.39	0.21	0.27	0.40	0.39	0.21	0.24	0.40	0.37	0.42	0.00

Fig. 2. Genetic distances between populations estimated from Y-haplogroup frequencies (from Sahoo et al. 2006).

of India, of people associated either with the development of agriculture or the spread of the Indo-Aryan language family. (Sahoo et al. 2006: 843)

The second of the two rejected associations is that of the Indo-Aryan expansion. The first, that of the spread of agriculture, is the well-known thesis of Colin Renfrew (1989), which traces Indo-European origins to the beginnings of agriculture in Anatolia and sees Indo-Europeans entering India around 9000 BP along with agriculture: Sahoo et al. see no evidence of this in the genetic record. (There are also considerable archaeological difficulties with Renfrew's thesis, both in and outside India; besides, recent evidence on the practice of agriculture in the Ganges Valley as early as in the eighth millennium points to an indigenous origin of Indian agriculture; however, a discussion of this issue is beyond the scope of this paper.)

The same data allow the authors to construct an eloquent table of genetic distances between several populations, based on Y-haplogroups (Fig. 2). We learn from it, for instance, that “the caste populations of ‘north’ and ‘south’ India are not particularly more closely related to each

other (average Fst value = 0.07) than they are to the tribal groups (average Fst value = 0.06)” (Sahoo et al. 2006: 844), an important confirmation of earlier studies. (Fst is, simply put, a measure of the degree of differentiation among populations; its values range from 0 to 1). In particular, “Southern castes and tribals are very similar to each other in their Y-chromosomal haplogroup compositions.” (Sahoo et al. 2006: 845) As a result, “it was not possible to confirm any of the purported differentiations between the caste and tribal pools” (Sahoo et al. 2006: 847)—which effectively negates the picture dictated by the Aryan paradigm of tribal *adivasis* vs. caste Hindus as descendants of Indo-Aryans immigrants. In reality, today we have no way to determine who in India is an “*adi*”-*vasi* (original inhabitant), but enough data to reject this label as misleading and unnecessarily divisive. Our whole notion of “tribe” in the Indian context, which anyhow carries a heavy colonial baggage, turns out to be deeply flawed, as a few Indian anthropologists had already pointed out (e.g., Singh 2011).

The same year, Noah A. Rosenberg directed a study on “Low Levels of Genetic Divergence

across Geographically and Linguistically Diverse Populations from India". It found that "genetic variation in India is distinctive with respect to the rest of the world, but that the level of genetic divergence is smaller in Indians than might be expected for such a geographically and linguistically diverse group" (Rosenberg et al. 2006: 2053), stressing again the subcontinent's genomic unity, in contrast with regions outside the subcontinent: "The noticeable genetic divergence of India from other regions is coupled with low levels of genetic divergence across the subgroups within India." (Rosenberg et al. 2006: 2053) Significantly (and keeping in mind that F_{st} is an index of genetic distance or differentiation).

Compared to groups that speak Indo-European languages, the groups in our study that speak Dravidian languages (Kannada, Malayalam, Tamil, and Telugu) did not show noticeably different patterns of pairwise F_{st} values, and in particular, they did not show a greater F_{st} from populations of Europe and the Middle East. Although a process of ancient admixture with indigenous Dravidian speakers by Indo-European populations originating to the west of India might have been expected to result in an elevated genetic distance from modern Dravidians to European and Middle Eastern populations, our analysis does not find evidence of such an admixture process. (Rosenberg et al. 2006: 2054-55)

This "admixture process" is the one that would have followed an Aryan invasion or immigration, and which the study failed to document. "However," it continued, "the admixture scenario is not directly contradicted: the data are compatible with a view in which the admixture occurred in such a manner that at its conclusion, similar contributions of ancestral Dravidians were present in the precursors of the

modern Dravidian-speaking and non-Dravidian-speaking groups of our study." In other terms, the "admixture" between the two linguistic groups, if it took place, could have resulted from repeated population contacts over a long time.

In 2007, Gyaneshwer Chaubey, together with M. Metspalu, T. Kivisild and R. Villems, reviewed many earlier studies, including some of those quoted above, and stressed the "caste-tribe continuum", as it is now called. The paper asked:

whether any of these can be singled out as more "autochthonous" than others. However ... this would be highly problematic, first, because the language families involved are generally believed to be far younger than the time frame required for the peopling of India. Secondly, such "autochthonous" Indian-specific mtDNA and Y chromosome lineage groups are widely spread across language borders in the subcontinent ... and the putative language shifts make it hard to infer the original tongue for every population studied even during the historic period and perhaps impossible for earlier times. Thus, the present-day linguistic affinities of different Indian populations per se are perhaps among the most ambiguous and even potentially controversial lines of evidence in the reconstruction of prehistoric demographic processes in India. (Chaubey et al. 2007: 97)

In lay terms, this means, once again, that current linguistic groups in India cannot be equated to corresponding ethnic groups: the demarcation lines do not coincide. The paper also agreed with earlier studies that "Most of the Indian-specific mtDNA haplogroups show coalescent times 40,000–60,000 YBP." (Chaubey et al. 2007: 97)

The same year, Phillip Endicott, together with Metspalu and Kivisild, took a closer look at the question of "modern human dispersals in South Asia". Their observation as regards India's

linguistic demarcation lines is an unambiguous rejection of the older paradigm:

The Austro-Asiatic and Tibeto-Burman language groups may retain a distinctive genetic signature due to their relatively recent introduction and limited subsequent male gene flow. However, consistent divisions between populations speaking Dravidian and Indo-Aryan languages are harder to define with reliability. The complex and intertwined history of changes in language, subsistence patterns, demography and political intervention, makes it difficult to relate genetic patterns to these widespread linguistic categories. The evidence from mtDNA argues against any strong differentiation between these (and other) major language groups ..., and therefore nullifies attempts to trace, maternally, the large-scale population movements once speculated to have accompanied the arrival of Indo-Aryan languages. (Endicott et al. 2007: 238)

In a 2008 paper, Peter A. Underhill warned against what he called “pitfalls” in interpreting the genetic data, in particular “a simplistic understanding of the seductive storyline provided by the Y chromosome” (Underhill 2008: 105). Without going into the technical intricacies involved, let us mention that Underhill is led to question the conventional view that Dravidian speakers originated from southwest Persia, a view that derived, among others, from the work of the U.S. linguist David W. McAlpin in the 1970s (see McAlpin 1981), which built upon perceived parallels between Dravidian and Elamite. Although often quoted as the last word on the origin of Dravidian speakers, McAlpin’s thesis had failed to convince some of his own colleagues, including experts on Dravidian linguistics (see Comments in McAlpin 1975; also Zvelebil 1990: 104-115). With a fresh look at the data from genetics, Underhill finds a haplogroup (called L1-M27), which forms an important component of genetic make-up of West Asian populations, “emanating from India

sometime after an initial colonization, in a polarity opposite that expected by the McAlpin model. ... This population subdivision occurred during pre-historical times and argues against an origin of Dravidian in the Iranian plateau and recent displacement southward by Indo-European agriculturists. The current data are more consistent with the Deccan origin model” (Underhill 2008: 108). In other words, Dravidian speakers appear to have originated within the Indian subcontinent, a view already proposed by the American archaeobotanist Dorian Fuller who, on the basis of archaeobotanical as well as linguistic evidence, opted for “proto-Dravidians somewhere within the core range of modern Dravidians... the main directions of dispersal would have been out from the Deccan towards its peripheries and zones of isolation” (Fuller 2003: 207-208).

BACK TO CASTE

The next year, the Indian geneticist Swarkar Sharma piloted a study on the vexed issue of the origins of the caste system. It reviewed and attempted to assess the competing theses in the field. Studying a sample of 681 Brahmins and 2128 tribals and Scheduled Castes, the authors found “no consistent pattern of the exclusive presence and distribution of Y-haplogroups to distinguish the higher-most caste, Brahmins, from the lower-most ones, schedule castes and tribals.” (Sharma et al. 2009: 51) In their view, the Y-haplogroup R1a1 held the key to the origins of the caste system; exploring its frequency not only in India but also in the rest of Eurasia and Central Asia in particular, they found that “the age of R1a1 was the highest in the Indian subcontinent” and concluded “in favor of the suggestion that there has been no bulk migration from Central Asia to India.” (Sharma et al. 2009: 54, 52) Their next observation was:

Interestingly, among different groups, the age of Y-haplogroup R1a1 was highest in scheduled castes/tribes when compared with Central Asians and Eurasians. These observations weaken the hypothesis of introduction of this haplogroup and the origin of Indian higher most castes from Central Asian and Eurasian regions, supporting their origin within the Indian subcontinent (Sharma et al. 2009: 54).

Their conclusion deserves to be quoted at some length:

The observation of R1a in high frequency for the first time in the literature, as well as analyses using different phylogenetic methods, resolved the controversy of the origin of R1a1, supporting its origin in the Indian subcontinent. Simultaneously, the presence of R1a1 in very high frequency in Brahmins, irrespective of linguistic and geographic affiliations, suggested it as the founder haplogroup for the population. The co-presence of this haplogroup in many of the tribal populations of India, its existence in high frequency in Saharia (present study) and Chenchu tribes, the high frequency of R1a in Kashmiri Pandits (KPs—Brahmins) as well as Saharia (tribe) and associated phylogenetic ages supported the autochthonous origin and tribal links of Indian Brahmins, confronting the concepts of recent Central Asian introduction and rank-related Eurasian contribution of the Indian caste system. (Sharma et al. 2009: 54)

This is an emphatic rejection of the Aryan scenario's views on the origins of caste, although the paper ended on a cautionary note calling for more representative samples.

In 2010, Underhill was the lead author of a study that examined the relationship between European and Asian Y chromosomes within the haplogroup R1a, which has been regarded as a marker of the supposed Indo-European migrations. The authors found that “coalescent time estimates of R1a1a correlate with the timing of the recession of the Last Glacial Maximum

and predate the upper bound of the age estimate of the Indo-European language tree. ... The presence and overall frequency of haplogroup R1a does not distinguish Indo-Iranian, Finno-Ugric, Dravidian or Turkic speakers from each other.” The earlier use of this marker for Indo-European migrations would thus be unjustified, unless proto-Indo-European can be pushed back beyond 10000 BC, which most linguists would be unwilling to accept. Moreover, the distribution of sub-haplogroups of R1a “would exclude any significant patrilineal gene flow from East Europe to Asia, at least since the mid-Holocene period” (Underhill et al. 2010: 483), precluding once again any significant migration from eastern Europe to Asia since about 4000 BC.

Significantly, the authors' study of frequency distribution for the haplogroup most commonly associated with Indo-European speakers, R1a1a (which, for our purpose, is the same as M17), differs from more conventional studies, but agrees with the preceding one (Sharma et al. 2009), in that it displaces the centre of gravity for this marker from eastern Europe or Central Asia to the Indian subcontinent (see Fig. 3).

For our most recent study, we turn again to Metspalu, who piloted in 2011 a study of 142 samples from 30 ethnic groups in India. The chief finding was that “Indian populations are characterized by two major ancestry components, one of which is spread at comparable frequency and haplotype diversity in populations of South and West Asia and the Caucasus. The second component is more restricted to South Asia and accounts for more than 50% of the ancestry in Indian populations” (Metspalu et al. 2011: 731). But the first component, shared with regions west of India, “cannot be explained by recent gene flow, such as the hypothetical Indo-Aryan migration”

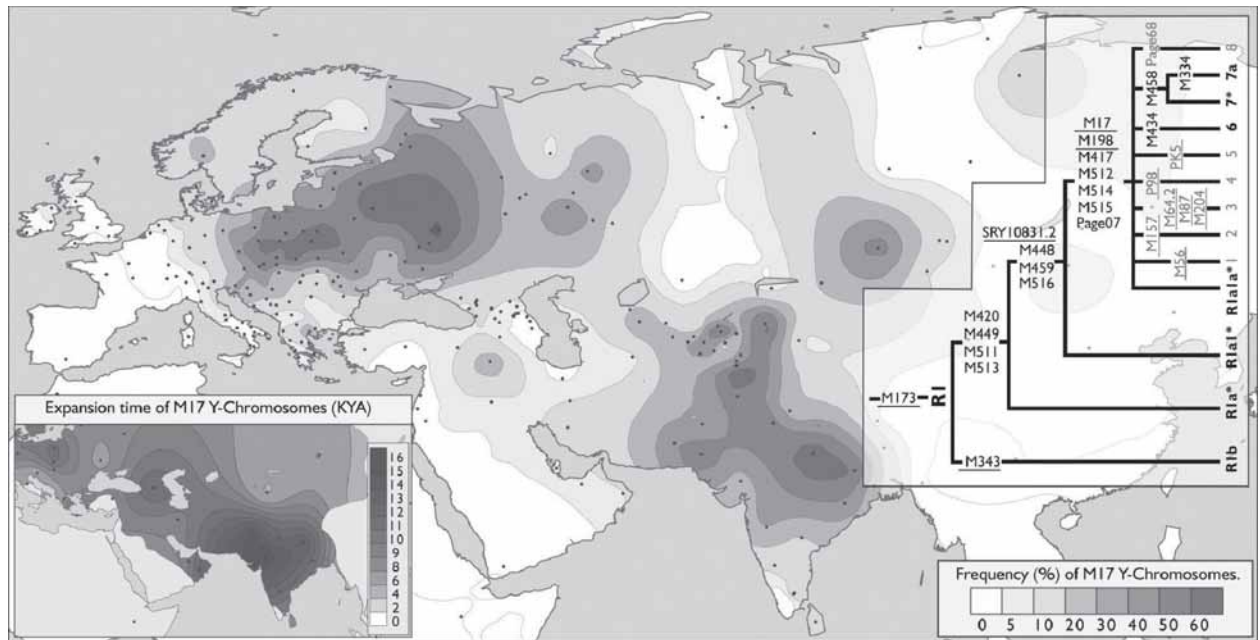


Fig. 3. Geographic distribution of haplogroup R1a1a frequency; see Underhill et al. 2010: 481 for detailed explanation.

(Metspalu et al. 2011: 740). The evidence, instead, “suggests multiple gene flows to the South Asian gene pool, both from the west and east, over a much longer time span” (Metspalu et al. 2011: 741). The authors also offered a welcome reminder of the complexity of genetic origins in the Indian context:

Several aspects of the nature of continuity and discontinuity of the genetic landscape of South Asia and West Eurasia still elude our understanding. Whereas the maternal gene pool of South Asia is dominated by autochthonous lineages, Y chromosome variants of the R1a clade are spread from India (ca 50%) to eastern Europe and their precise origin in space or time is still not well understood (Metspalu et al. 2011: 739).

DIVERGING VIEWS

Despite the above barrage of studies challenging the conventional scenario, geneticists are yet to reach unanimity about the origins of Indian populations. Thus a 2001 study directed by the

U.S. biologist Michael Bamshad found that “upper castes are more similar to Europeans than to Asians” and concluded that “Y-chromosome variation confirms Indo-European admixture” (Bamshad et al. 2001). Such conclusions were soon cited (not without some glee) as proof of the Aryan migration theory, until they were swept away by later studies.

The same year, the Indian geneticist Partha P. Majumder acknowledged the “fundamental unity of mtDNA lineages in India in spite of the extensive cultural and linguistic diversity” (Majumder 2001: 535), but, citing Romila Thapar, remained committed to the view that “pastoral nomads originating in the Central Asian steppes may also have contributed to the gene pool of India. The entry of humans from these regions into India was through the northwest corridor of India. ... It is known that after the entry of the Aryan-speakers into India, the Brahmins were the torch-bearers and promoters of Aryan rituals” (Majumdar 2001: 541-44). In a more recent

study, Majumdar repeated the same methodological error, basing himself on the belief that there was “a conquest of this region [the Northwest] by nomadic people from Central Asia, who spoke Indo-European languages. This conquest by Indo-European speakers introduced a social structure that is hierarchical (the caste system), and persists even to this day” (Majumdar 2008: 280). Additionally, he invoked obsolete linguistic evidence such as the existence of “the existence of a solitary Dravidian-speaking group, the Brahui” as evidence for the spread of Dravidian speakers into South Asia, unaware of the fact that Brahui has long been shown to be a recent entrant into Baluchistan (see references in Danino 2009: 76-77). Similarly, the notion of a “proto-Elamo-Dravidian language” (Majumdar 2008: 282) refers to the above-mentioned thesis by McAlpin, which as we saw stands challenged by genetics and archaeobotany. This shows the danger of trying to suit the genetic evidence to predetermined theories instead of letting it speak on its own terms. However, in a recent popular article, Majumdar adopted a more cautious line: “The initial view that there was large-scale migration from Central Asia into India has been significantly modulated.” (Majumdar and Balasubramanian 2009: 76)

The same pattern can be found in the 2004 study directed by the French geneticist Richard Cordaux, who argued that “paternal lineages of Indian caste groups are primarily descended from Indo-European speakers who migrated from Central Asia 3,500 years ago. Conversely, paternal lineages of tribal groups are predominantly derived from the original Indian gene pool.” (Cordaux et al. 2004: 231) But the precision of the date is suspect, and the only evidence provided for the said migration was that “archaeological and linguistic evidence

support” it. Quite the contrary, as mentioned earlier, archaeological evidence actually runs against the migrationist view, while linguistic evidence is ambivalent and can be explained through non-diffusionist models. The authors do not seem to have realized the circularity of their approach, accepting the supposed Indo-European migration and suiting the genetic evidence to it.

In 2008, a study entitled “Genetic landscape of the people of India: a canvas for disease gene exploration” was published by the Indian Genome Variation Consortium (with seven co-authors and some 150 collaborators); its primary focus was to identify “markers on disease or drug-response related genes in diverse populations”. However, it did remark on the connection between linguistic and ethnic groups, noting “high levels of genetic divergence between groups of populations that cluster largely on the basis of ethnicity and language” (Indian Genome Variation Consortium 2008: 3), while most of the above-mentioned studies saw no such coincidence between genetic and linguistic clusters. Again, “We observed that on a pan-India level, the tribal and caste populations are significantly differentiated. Besides, within some geographical regions, tribes and castes subclassified by language are also well differentiated” (Indian Genome Variation Consortium 2008: 11), in apparent contradiction to the above caste-tribe continuum. It is difficult to decide whether there is an absolute criterion for such “differentiations” or if they are a matter of relative emphasis and ultimately personal inclinations. Finally, the authors, referring to Romila Thapar’s *History of India* of 1966, write: “It is contented that the Dravidian speakers, now geographically confined to southern India, were more widespread throughout India prior to the arrival of the Indo-European speakers. They,

possibly after a period of social and genetic admixture with the Indo-Europeans, retreated to southern India.... Our results showing genetic heterogeneity among the Dravidian speakers further supports the above hypothesis. The Indo-European speakers also exhibit a similar or higher degree of genetic heterogeneity possibly because of different extents of admixture with the indigenous populations over different time periods after their entry into India.” (Indian Genome Variation Consortium 2008: 9-10) This is another clear case of circularity: a now discarded thesis is accepted *a priori* and “genetic heterogeneity” interpreted along those lines in disregard of more likely alternatives: if those populations were long settled in India, limited population movements and complex interactions (not just from north to south) since Palaeolithic times could easily account for “genetic heterogeneity among the Dravidian speakers”. Such methodological flaws are not expected of a scientific study of this standard.

Another differing view was published in *Nature* in 2009. An Indo-U.S. team directed by David Reich introduced the concepts of “Ancestral North Indians” (ANI) and “Ancestral South Indians” (ASI) and found them “genetically divergent”. For instance, the ANI were found to be “genetically close to Middle Easterners, Central Asians, and Europeans” and “ANI ancestry ranges from 39-71% in most Indian groups, and is higher in traditionally upper caste and Indo-European speakers.” (Reich et al. 2009: 489) Although the study noted degrees of “ANI-ASI mixture”, it found it “tempting to assume that the population ancestral to ANI and CEU spoke ‘Proto-Indo-European’, which has been reconstructed as ancestral to both Sanskrit and European languages, although we cannot be certain without a date for ANI-ASI mixture.” (Reich et al. 2009: 492) Apart from the *a priori*

acceptance, again, of a “tempting” linguistic theory, the study did not offer a date for the proposed separation of ANI from European populations. Moreover, its statistical methods are very elaborate and need to be tested by other workers in the field. For instance, whether its populations samples were adequate is doubtful: although the study involved 25 Indian populations, it was far from representative: many Indian states were completely left out (Himachal Pradesh, Punjab, Haryana, Bihar, West Bengal, Orissa, Maharashtra, Tamil Nadu and a few Northeastern states) or represented by a single population (Jammu & Kashmir, Uttaranchal, Rajasthan, Gujarat, Madhya Pradesh, Jharkhand, Chattisgarh, Kerala). With such a poor distribution, it is hard to take seriously the concepts of ANI and ASI, which, moreover, are hardly defined; it may be asked whether introducing them does not also introduce an artificial division among Indian populations. The authors were however careful enough to qualify their conclusions:

We warn that “models” in population genetics should be treated with caution. Although they provide an important framework for testing historical hypotheses, they are oversimplifications. For example, the true ancestral populations of India were probably not homogeneous as we assume in our model, but instead were probably formed by clusters of related groups that mixed at different times. (Reich et al. 2009: 492)

More examples of methodological flaws in genetics studies were discussed by Nicole Boivin in 2007:

In reading the genetics literature on South Asia, it is very clear that many of the studies actually start out with some assumptions that are clearly problematic, if not in some cases completely untenable. Perhaps

the single most serious problem concerns the assumption, which many studies actually start with as a basic premise ... that the Indo-Aryan invasions are a well-established (pre)historical reality. (Boivin 2007: 352)

Boivin discusses this flaw in several studies, such as Bamshad et al. 2001 or Cordaux et al. 2004 cited above, pointing out that they “confirm such invasions in large part because they actually assume them to begin with.” (Boivin 2007: 352) Among other methodological issues, she notes the failure to take into account the genetic legacy of known invasions, especially of historical periods, and the “problematic assumption ... that caste is unchanging”, e.g. that today’s Brahmin necessarily had Brahmin ancestors, which need not be correct, or again that castes were strictly endogamous, which is rarely the case (Boivin 2007: 354). In other words, genetics studies ignoring the fluidity of the social entities going by the name of castes are likely to reach erroneous conclusions.

CONCLUSIONS

Genetics of human populations is a relatively young discipline, which, in the Indian context, has to contend with an acknowledged diversity as well as complexity. We are still far from being able to re-create a comprehensive genetic history of Indian populations. In the meantime, let us sum up the main conclusions reached by the first group of sixteen studies examined in this chapter as far as the Aryan debate is concerned:

- A rejection of the addition to Indian populations of a “Caucasoid” or Central Asian gene pool about 1500 BC, and the assertion of an indigenous origin for most Indian populations, including upper castes. Just as the putative Aryan

immigration left no trace in Indian literature, in the archaeological and the anthropological record, it is undetectable at the genetic level—unless *a priori* assumed to be true.

- A rejection of facile and largely colonial assumptions that tribal groups are descendants of India’s “original” inhabitants (*adivasis*), while Dravidian as well as Indo-European speakers have later entrants as ancestors.
- A rejection of a sharp genetic demarcation line between tribal and caste populations: there is no significant (or, at least, definable) genetic pattern to differentiate Brahmins, Dalits and tribals, all of whom may be regarded as autochthonous in origin.

Besides, India’s considerable genetic diversity can make sense only by using a time-scale not of a few millennia, but of 40,000 to 60,000 years. In fact, several studies, such as Stephen Oppenheimer (2003), Lluís Quintana-Murci et al. (2004), Vincent Macaulay et al. (2005), Hannah V.A. James and Michael D. Petraglia (2005), have in the last few years proposed that modern humans migrating out of Africa first reached southwest Asia around 75,000 BP, and from here, went on to other parts of the world. In simple terms, except for Africans, all humans would have ancestors there. In particular, one migration started around 50,000 BP towards the Middle East and Western Europe:

Indeed, nearly all Europeans—and by extension, many Americans—can trace their ancestors to only four mtDNA lines, which appeared between 10,000 and 50,000 years ago and originated from South Asia. (Allman 2004)

Oppenheimer, a leading advocate of this scenario, summarizes it in these words:

For me and for Toomas Kivisild, South Asia is logically the ultimate origin of M17 and his ancestors; and sure enough we find the highest rates and greatest diversity of the M17 line in Pakistan, India, and eastern Iran, and low rates in the Caucasus. M17 is not only more diverse in South Asia than in Central Asia, but diversity characterizes its presence in isolated tribal groups in the south, thus undermining any theory of M17 as a marker of a 'male Aryan invasion' of India. One average estimate for the origin of this line in India is as much as 51,000 years. All this suggests that M17 could have found his way initially from India or Pakistan, through Kashmir, then via Central Asia and Russia, before finally coming into Europe. (Oppenheimer 2003: 152)

This would mean that India acted "as an incubator of early genetic differentiation of modern humans moving out of Africa." (Kivisild et al. 2003b: 327) Endicott's study quoted earlier also argued in favour of:

a rapid dispersal of modern humans from eastern Africa and subsequent settlement of South Asia. A single exodus along a southern, possibly coastal, route is a parsimonious conclusion to draw from contemporary patterns of haploid genetic distribution and diversity. ... The population movements of the Holocene, together with the appearance of West Eurasian mtDNA lineages in the period 40–20 ka, indicate that South Asia has indeed been "at the crossroads" for much of modern

human prehistory, but that the autochthonous elements of its genetic heritage have not been dominated by these later comings and goings. (Endicott et al. 2007: 240)

In the authors' opinion, more refined studies based on larger population samples "will continue to emphasize the genetically complex patterns present, and are increasingly unlikely to support reductionist explanations of simplistic demographic and cultural scenarios. Rather, they should put weight behind the suggestion that West and South Asia, as conduits for the settlement of the rest of the world, are central to comprehending modern human evolution outside of Africa." (Endicott et al. 2007: 240)

Genetics is a fast-evolving discipline, and while we must expect frequent new developments to gradually build up a synthetic view of the origins of Indian populations, it is certain that we will never have to return to the nineteenth-century racial fallacies of waves of Aryan migrants driving tribal autochthons into the hills or Dravidian speakers southward. Such entities have no reality in genetic, bioanthropological, archaeological or cultural terms. In this sense, genetics is joining other disciplines in helping to clean the cobwebs of colonial historiography.

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